means for determining positions of said plurality of partial sequences related to each one of said different DNA nucleotide sequences, each of said plurality of different partial sequences being extracted from different exons;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for determining;

means for determining a plurality of pairs of primers for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with genetic functions related to said different DNA nucleotide sequences respectively.

C1 concld

C2

7. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of human genomes, said program comprising instructions

SUB D6

for reading data on a plurality of different DNA nucleotide sequences in said memory,

for extracting a plurality of partial sequences meeting extraction conditions from said plurality of different DNA nucleotide sequences and the data on said plurality of different DNA nucleotide sequences, wherein said extraction conditions including a predetermined base length,

for determining positions of said plurality of partial sequences related to each one of said different DNA nucleotide sequences, each of said plurality of different partial sequences being extracted from different exons,

for selecting a plurality of different partial sequences from results of the determining step, and

for determining a plurality pairs of primers for each of said plurality of different partial sequences, and

for automatically collating said plurality of pairs of primers with genetic functions related to said different DNA nucleotide sequences respectively.

8. A method for designing primers, comprising the steps of:

(a) taking data on a plurality of different DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences of human genomes;

(b) extracting a plurality of partial sequences meeting extraction conditions from each of said plurality of different DNA nucleotide sequences based on said data , wherein said extraction conditions including a predetermined base length;

(c) determining positions of said plurality of partial sequences related to each one of said plurality of different DNA nucleotide sequences;

(d) selecting a plurality of different partial sequences from said plurality of partial sequences, each of said plurality of different partial sequences being extracted from different exons;

(e) after the step (d), determining a plurality pairs of primers for each of said plurality of different partial sequences, and

C2 concld

(f) automatically collating said plurality of pairs of primers with genetic functions related to said different DNA nucleotide sequences respectively.

C3

11. A method for designing primers, comprising the steps of

(a) taking data on a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of human genomes;

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(b) extracting a plurality of partial sequences meeting extraction conditions from each of said plurality of different DNA nucleotide sequences based on said data , wherein said extraction conditions including a predetermined base length;

(c) determining certain conditions related to positions of said plurality of partial sequences related to each one of said plurality of different DNA nucleotide sequences;

(d) selecting a plurality of different partial sequences from said plurality of partial sequences], each of said plurality of different partial sequences being extracted from different exons;

(e) after the step (d), determining a plurality pairs of primers for each of said plurality of different partial sequences; and

(f) analyzing a sample DNA using as an indicator the type of primer affording PCR amplified fragments among said plurality of primers with a storage medium,

wherein said storage medium comprises recorded data on said plurality pairs of primers, genetic data on DNA fragments amplified by PCR using said plurality pairs of primers, and said plurality of pairs of primers automatically collated with genetic functions related to said different DNA nucleotide sequences.

19. A primer design system, comprising:

means for selecting a plurality of different DNA nucleotide sequences based on at least one predetermined genetic function of interest from a database having data on a plurality of DNA nucleotide sequences of human genomes; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting certain base length extraction conditions from the plurality of different DNA nucleotide sequences;

means for determining positions of said plurality of partial sequences related to each one of said plurality of different DNA nucleotide sequences;

means for selecting a plurality of different partial sequences from said plurality of partial sequences, each of said plurality of different partial sequences being extracted from different exons; and

means for determining a plurality pairs of primers for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said genetic functions of interest related to said different DNA nucleotide sequences respectively.

Please add new claims 20-29 as follows:

20. A primer design system, comprising:

means for selecting a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of human genomes; and

a control unit for controlling the system, said control unit controlling:

means for positioning exons associated with genetic functions of interest on the plurality of different DNA nucleotide sequences;

means for extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions including a predetermined base length;

means for collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

means for determining a plurality of pairs of primers for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with the genetic functions and the positions related to said different DNA nucleotide sequences respectively.

21. A primer design system according to claim 20 further comprising means for selecting the exons associated with genetic functions of interest by at least one of:

(a) meeting a predetermined base length;

(b) predicting with an exon predicting program;

(c) from at least one EST database;

(d) from at least one EST database and having a SNP potential;

(e) from at least one protein database and having no known protein function.

C5 contd

22. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of human genomes, said program comprising instructions

SUB D10

for reading data on a plurality of different DNA nucleotide sequences in said memory;

for positioning exons associated with genetic functions of interest on the plurality of different DNA nucleotide sequences;

for extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions including a predetermined base length;

for collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

for determining a plurality of pairs of primers for each of said plurality of different partial sequences; and

for automatically collating said plurality of pairs of primers with the genetic functions and the positions related to said different DNA nucleotide sequences respectively.

23. A storage medium according to claim 22, wherein said program further comprising instructions for selecting the exons associated with genetic functions of interest by at least one of:

(a) meeting a predetermined base length;

(b) predicting with an exon predicting program;

(c) from at least one EST database;

(d) from at least one EST database and having a SNP potential;

(e) from at least one protein database and having no known protein function.

24. A method for designing primers, comprising:

(a) selecting a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of human genomes;

(b) positioning exons associated with genetic functions of interest on the plurality of different DNA nucleotide sequences;

(c) extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions including a predetermined base length;

(d) collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

(e) selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

(f) determining a plurality of pairs of primers for each of said plurality of different partial sequences; and

(g) automatically collating said plurality of pairs of primers with the genetic functions and the positions related to said different DNA nucleotide sequences respectively.

25. A method for designing primers according to claim 24 further comprising selecting the exons associated with genetic functions of interest by at least one of:

(a) meeting a predetermined base length;

(b) predicting with an exon predicting program;

(c) from at least one EST database;

(d) from at least one EST database and having a SNP potential;

(e) from at least one protein database and having no known protein function.

26. A method for designing primers, comprising:

(a) selecting a plurality of different DNA nucleotide sequences from a database including a plurality of DNA nucleotide sequences of human genomes;

C5 cont'd

(b) positioning exons associated with genetic functions of interest on the plurality of different DNA nucleotide sequences;

(c) extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions including a predetermined base length;

(d) collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

(e) selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

(f) determining a plurality of pairs of primers for each of said plurality of different partial sequences; and

(f) analyzing a sample DNA using as an indicator the type of primer affording PCR amplified fragments among said plurality of primers with a storage medium,

wherein said storage medium comprises recorded data on said plurality pairs of primers, genetic data on DNA fragments amplified by PCR using said plurality pairs of primers, and said plurality of pairs of primers automatically collated with genetic functions related to said different DNA nucleotide sequences.

27. A method for designing primers according to claim 26 further comprising selecting the exons associated with genetic functions of interest by at least one of:

(a) meeting a predetermined base length;

(b) predicting with an exon predicting program;

(c) from at least one EST database;

(d) from at least one EST database and having a SNP potential;

(e) from at least one protein database and having no known protein function.

28. A primer design system, comprising:

SUB D12

means for selecting a plurality of different DNA nucleotide sequences based on at least one predetermined genetic function of interest from a database having data on a plurality of DNA nucleotide sequences of human genomes; and

a control unit for controlling the system, said control unit controlling:

means for positioning exons associated with the genetic function of interest on the plurality of different DNA nucleotide sequences;

means for extracting a plurality of partial sequences from the exons under extraction conditions, wherein said extraction conditions including a predetermined base length;

means for collating positions of said plurality of partial sequences related to each of the exons and the genetic functions;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

means for determining a plurality of pairs of primers for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with the genetic functions and the positions related to said different DNA nucleotide sequences respectively.

29. A primer design system according to claim 28 further comprising means for selecting the exons associated with the genetic function of interest by at least one of:

(a) meeting a predetermined base length;

(b) predicting with an exon predicting program;

(c) from at least one EST database;

(d) from at least one EST database and having a SNP potential;

(e) from at least one protein database and having no known protein function.

C5 cond d